

OIPE

RAW SEQUENCE LISTING DATE: 06/16/2000  
PATENT APPLICATION: US/09/589,870 TIME: 11:34:25

**Input Set : A:\547.app**  
**Output Set: N:\CRF3\06162000\1589870.raw**

4 <110> APPLICANT: Goshorn, Stephen C.  
5       Graves, Scott Stoll  
6       Schultz, Joanne Elaine  
7       Lin, Yakang  
8       Sanderson, James A.  
9       Reno, Jonh M.  
11 <120> TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
12 METHODS OF USE THEREOF  
15 <130> FILE REFERENCE: 690022.547  
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/589,870  
18 <141> CURRENT FILING DATE: 2000-06-05  
20 <160> NUMBER OF SEQ ID NOS: 46  
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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25 <211> LENGTH: 638  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Streptomyces avidinii  
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31 cgtcggtcga gccatcgccg tttccctgac cacggctcga attacggcca gcgcttcggc  
32 agacccctcc aaggactcga aggcccagggt ctgcggccgc gagggccggca tcaccggcac  
33 ctggatcaac cagtcggct cgaccttcat ctgtacccggc ggccggccggc ggcggcttgcac  
34 cggaaacctac gaggatccac cggatccggc tcggcaacgc cgagggccgc taatgttgcggc  
35 cggacggcgc cccggccaccc acggcggccggc caccggccctc ggttggacgg tgccctggaa  
36 gaataactac cgcaacggcc actccggcgc acgttgagc ggcagttacgc tggcgccgc  
37 cgaggcgagg atcaacaccc agtggctgt gacccctggc accaccgggg ccaacgcctg  
38 gaagtccacac ctggatccggc acgacacccat caccatgggg aatggcgccgg ccgccttccat  
39 cggacggcgc aagaaggccggc ggttcaacaa cggcaacccgg ctcgacggcgttccggat  
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43 <211> LENGTH: 183  
44 <212> TYPE: PRT  
45 <213> ORGANISM: Streptomyces avidinii  
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50 Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala  
51       20                         25                                 30  
52 Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln  
53       35                         40                                 45  
54 Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr  
55       50                         55                                 60  
56 Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu  
57       65                         70                                 75                             80  
58 Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala  
59       85                         90                                 95  
60 Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser

**ENTERED**

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61      100          105          110
62 Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile
63      115          120          125
64 Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp
65      130          135          140
66 Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser
67 145      150          155          160
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75 <212> TYPE: DNA
76 <213> ORGANISM: Streptomyces avidinii
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81 ccatcgaccg ggacctcgac catccaggatc tgccgcacaa gacacatgcc gcactgctgt 180
82 ttgttcaccc acaccgtcg gtgcacggcc gaggtcacaa accttgacgg gcgggatacg 240
83 gacggcgcac gccacagcgc gccctccgtc cccgcgggc aacaactagg gagtatttt 300
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85 gattacggcc atggctgaca tcaggatgac tcagtctcca tcgtcctgt ctgcctctgt 420
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91 cgggtgtggg tgggtggcg gaggctcgag ccaggttcag ctggtccagt ctggggcaga 780
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101 cacggacggc agcggcaccg ccctcggtt gacgggtggcc tggaaagaata actaccgaa 1380
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104 cggccacgac accttcacca agtgaagcc gtccggccgc tccatcgacg cggcgaagaa 1560
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108 <211> LENGTH: 431
109 <212> TYPE: PRT
110 <213> ORGANISM: Streptomyces avidinii
112 <400> SEQUENCE: 4
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114	1	5	10	15
115	Ser Ile Thr Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser			
116	20	25	30	
117	Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser			
118	35	40	45	
119	Gln Gly Ile Arg Gly Asn Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys			
120	50	55	60	
121	Gly Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val			
122	65	70	75	80
123	Pro Ser Arg Phe Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr			
124	85	90	95	
125	Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln			
126	100	105	110	
127	Arg Asn Ala Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile			
128	115	120	125	
129	Lys Ile Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly			
130	130	135	140	
131	Gly Ser Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
132	145	150	155	160
133	Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile			
134	165	170	175	
135	Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
136	180	185	190	
137	Gln Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Ser Asp			
138	195	200	205	
139	Leu Ser Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn			
140	210	215	220	
141	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val			
142	225	230	235	240
143	Tyr Tyr Cys Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr			
144	245	250	255	
145	Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Ala			
146	260	265	270	
147	Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly			
148	275	280	285	
149	Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr			
150	290	295	300	
151	Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly			
152	305	310	315	320
153	Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro			
154	325	330	335	
155	Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys			
156	340	345	350	
157	Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr			
158	355	360	365	
159	Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser			
160	370	375	380	
161	Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp			
162	385	390	395	400

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163 Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys  
 164 405 410 415  
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 169 <211> LENGTH: 1239  
 170 <212> TYPE: DNA  
 171 <213> ORGANISM: Streptomyces avidinii  
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 176 tcctccccca aacctttggat ttatgcacca tccaaacctgg cctctggagt ccctgtcgc 180  
 177 tcctggca gtgggtctgg gacctttac ttcttcacaa tcagcagtg ggaggctgaa 240  
 178 gatgtgcctt ctttattactg ccagcagtgg attagtaacc caccacgtt cgggtctggg 300  
 179 accaagctgg agctgaagat ctctggctgg gaaggcagcc cggaagcagg tctgtctccg 360  
 180 gacgcagggtt ccggcgtcgag ccagggttcag ctggtcccatc caggggttgc gctgtgtaaag 420  
 181 cctggggctt cagtgaagat gcttgcacatc acatattac cagtttacat 480  
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 183 ggaatggtg atacttccata caatcagaag ttcaaaaggca aggccacatt gactgcagac 600  
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 187 gcccaggctt cggccggccga ggccggcatac accggcacctt ggttacaacca gcttggctcg 840  
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 189 ggcacacggcc agacggccgtt ctgttgcacc ggttgcgttac agacgcggccccc ggccacccgac 960  
 190 ggcacggcc acggcccttggg tggggatggtgc ggttgcggaa ataaacttccg caaccccccac 1020  
 191 tccgcgacca ctgttgcgggg ccagttacgtt ggcggcgcgg aggccaggat caacaccccg 1080  
 192 tggctgttgc cttccggcacc caccggggcc aacgccttgc agttccacgtt ggttgcggcacc 1140  
 193 gacacccatc ccaagggttgc ggcgttgcggcc gcttccatcg acgcggccgaa gaaggccggc 1200  
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 197 <211> LENGTH: 412  
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 201 <400> SEQUENCE: 6  
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 206 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr  
 207 35 40 45  
 208 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 209 50 55 60  
 210 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu  
 211 65 70 75 80  
 212 Asp Ala Ala Thr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr  
 213 85 90 95  
 214 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ile Ser Gly Leu Glu Gly  
 215 100 105 110

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216 Ser Pro Glu Ala Gly Leu Ser Pro Asp Ala Gly Ser Gly Ser Ser Gln
217      115          120          125
218 Val Gln Leu Val Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
219      130          135          140
220 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn
221 145          150          155          160
222 Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly
223      165          170          175
224 Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys
225      180          185          190
226 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
227      195          200          205
228 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
229      210          215          220
230 Arg Ala Gln Leu Arg Pro Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala
231 225          230          235          240
232 Gly Thr Thr Val Thr Val Ser Ser Gly Ser Gly Ser Ala Asp Pro Ser
233      245          250          255
234 Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly
235      260          265          270
236 Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala
237      275          280          285
238 Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu
239      290          295          300
240 Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp
241 305          310          315          320
242 Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr
243      325          330          335
244 Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly
245      340          345          350
246 Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr
247      355          360          365
248 Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr
249      370          375          380
250 Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly
251 385          390          395          400
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253      405          410
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263 agcagacacc tggacaggcc ctggaaatggta ttggagctat ttatccagga aatggtgata    180
264 cttcctacaa tcagaaggttc aaaggcaagg ccacattgac tgcagacaaa tcctccagca    240
265 cagcctacat gcagctcagc agcctgacat ctgaggactc tgcggcttat tactgtcaa    300
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**VERIFICATION SUMMARY** DATE: 06/16/2000  
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L:17 M:270 C: Current Application Number differs, Wrong Format